

VARIANT CATEGORIES				
Variant	Description	Patient Class	Gene Selection Criteria	Reference
rLGD	<u>r</u> ecurrent <u>L</u> ikely <u>G</u> ene <u>D</u> isrupting	ASD SCZ	genes harboring loss-of-function mutations, via nonsense, splice-site, or frameshift, that were identified in at least two probands	lossifov et al. (4) Fromer et al. (5) Gulsuner et al. (7) McCarthy et al. (8)
rdNS	<u>r</u> ecurrent <u>d</u> amaging <u>N</u> on- <u>S</u> ynonymous	SCZ	1) genes harboring damaging missense* mutations identified in at least two probands, or 2) genes harboring an LGD mutation in one proband in combination with a damaging missense mutation identified in at least one additional proband	Guipponi et al. (6) McCarthy et al. (8)
RVIS	<u>R</u> esidual <u>V</u> ariation <u>I</u> ntolerance <u>S</u> core	SCZ	genes harboring an LGD or broadly damaging missense [†] mutation and whose RVIS scores placed them in the top 15% of genes that have the least common functional genetic variation and are "intolerant"	McCarthy et al. (8)
SYN-NET ^{LGD}	<u>S</u> ynaptic <u>N</u> etwork- <u>L</u> GD	SCZ	genes harboring non-recurrent LGD mutations that were placed in a synaptic protein interaction network using SynSysNet database	Fromer et al. (5) Gulsuner et al. (7)
SYN-NET ^{MIS}	<u>S</u> ynaptic <u>N</u> etwork- <u>M</u> issense	SCZ	genes harboring missense [‡] mutations that were placed in a synaptic protein interaction network using SynSysNet database	Fromer et al. (5)
<p>(1) * damaging missense: a missense mutation predicted to be damaging by 2 prediction algorithms (SIFT, PolyPhen2). (2) [†] broadly damaging missense: a missense mutation predicted to be damaging by ≥1 prediction algorithm (SIFT, PolyPhen2, LRT, MutationTester). (3) [‡] missense: a mutation which induces a change in the amino acid sequence.</p>				